

Figure 1. 158P1D7 SSH sequence (SEQ ID NO:655).

```
1  GATCTGATAA GCTTTCAATG TTGCGCTCCT GACAATGTAT TAGAAGTCCT GATGGGGATA
61 GGACTTTGCA GTTACAAGGA ATAGGGCAGA AAGGTCCTGG AAGTTGAGTG GATGGCTTTG
121 TAATATAAGG TATCAAACCT GGTGCTTTGG TGGGTAGTTT TAGAATGGAC GTGGTCTTAG
181 TTGACATGCG ACTATCATTT ATTGAAGATG TTGCTGCCAG ATGTAATGAT C
```

158P1D7 SSH sequence

Figure 2. 158P1D7 cDNA clone TurboScript3PX and open reading frame (ORF)

1 M K L W I H L F Y S S L L
 1 tcggattttcatcacatgacaacATGAAGCTGTGGATTTCATCTCTTTTATTTCATCTCTCCT
 14 A C I S L H S Q T P V L S S R G S C D S
 61 TGCCTGTATATCTTTACACTCCCAAACCTCCAGTGTCTCATCCAGAGGCTCTTGTGATTG
 34 L C N C E E K D G T M L I N C E A K G I
 121 TCTTTGCAATTGTGAGGAAAAAGATGGCACAATGCTAATAAATTGTGAAGCAAAAGGTAT
 54 K M V S E I S V P P S R P F Q L S L L N
 181 CAAGATGGTATCTGAAATAAGTGTGCCACCATCACGACCTTTCCAACCTAAGCTTATTA
 74 N G L T M L H T N D F S G L T N A I S I
 241 TAACGGCTTGACGATGCTTCACACAAATGACTTTTCTGGGCTTACCAATGCTATTTCAAT
 94 H L G F N N I A D I E I G A F N G L G L
 301 ACACCTTGGATTAAACAATATTGCAGATATTGAGATAGGTGCATTTAATGGCCTTGGCCT
 114 L K Q L H I N H N S L E I L K E D T F H
 361 CCTGAAACAACCTTCATATCAATCACAATTCTTTAGAAATTCTTAAAGAGGATACTTTCCA
 134 G L E N L E F L Q A D N N F I T V I E P
 421 TGGACTGGAAAACCTGGAATTCCTGCAAGCAGATAACAATTTTATCACAGTGATTGAACC
 154 S A F S K L N R L K V L I L N D N A I E
 481 AAGTGCCTTTAGCAAGCTCAACAGACTCAAAGTGTTAATTTTAAATGACAATGCTATTGA
 174 S L P P N I F R F V P L T H L D L R G N
 541 GAGTCTTCCTCCAAACATCTTCCGATTTGTTCTTTAACCCTATCTAGATCTTCGTGGAAA
 194 Q L Q T L P Y V G F L E H I G R I L D C
 601 TCAATTACAAACATTGCCTTATGTTGGTTTCTCGAACACATTGGCCGAATATTGGATCT
 214 Q L E D N K W A C N C D L L Q L K T W L
 661 TCAGTTGGAGGACAACAAATGGGCCTGCAATTGTGACTTATTGCAGTTAAAACTTGGTT
 234 E N M P P Q S I I G D V V C N S P P F F
 721 GGAGAACATGCCTCCACAGTCTATAATTGGTGATGTTGTCTGCAACAGCCCTCCATTTT
 254 K G S I L S R L K K E S I C P T P P V Y
 781 TAAAGGAAGTATACTCAGTAGACTAAAGAAGGAATCTATTTGCCCTACTCCACCAGTGTA
 274 E E H E D P S G S L H L A A T S S I N D
 841 TGAAGAACATGAGGATCCTTCAGGATCATTACATCTGGCAGCAACATCTTCAATAAATGA
 294 S R M S T K T T S I L K L P T K A P G L
 901 TAGTCGCATGTCAACTAAGACCACGTCCATTCTAAAACCTACCCACCAAAGCACCAGGTTT
 314 I P Y I T K P S T Q L P G P Y C P I P C
 961 GATACCTTATATTACAAAGCCATCCACTCAACTTCCAGGACCTTACTGCCCTATTCTCTG
 334 N C K V L S P S G L L I H C Q E R N I E
 1021 TAACTGCAAAGTCCATCCCCATCAGGACTTCTAATACATTGTCAGGAGCGCAACATTGA
 354 S L S D L R P P P Q N P R K L I L A G N
 1081 AAGCTTATCAGATCTGAGACCTCCTCCGAAAATCCTAGAAAGCTCATTCTAGCGGGAAA
 374 I I H S L M K S D L V E Y F T L E M L H
 1141 TATTATTCACAGTTTAAATGAAGTCTGATCTAGTGAATATTTCACTTTGGAAATGCTTCA
 394 L G N N R I E V L E E G S F M N L T R L
 1201 CTTGGGAAACAATCGTATTGAAGTCTTGAAGAAGGATCGTTTATGAACCTAACGAGATT
 414 Q K L Y L N G N H L T K L S K G M F L G
 1261 ACAAAAACCTCTATCTAAATGGTAACCACCTGACCAAATTAAGTAAAGGCATGTTCTCTGG
 434 L H N L E Y L Y L E Y N A I K E I L P G
 1321 TCTCCATAATCTTGAATACTTATATCTTGAATACAATGCCATTAAGGAAATACTGCCAGG
 454 T F N P M P K L K V L Y L N N N L L Q V
 1381 AACCTTTAATCCAATGCCTAAACTTAAAGTCTGTATTTAAATAACAACCTCCTCCAAGT
 474 L P P H I F S G V P L T K V N L K T N Q
 1441 TTTACCACCACATATTTTTTTCAGGGGTTCTCTAACTAAGGTAAATCTTAAACAAACCA
 494 F T H L P V S N I L D D L D L L T Q I D
 1501 GTTTACCCATCTACCTGTAAGTAATATTTTGGATGATCTTGATTACTAACCAGATTGA
 514 L E D N P W D C S C D L V G L Q Q W I Q

1561 CCTTGAGGATAACCCCTGGGACTGCTCCTGTGACCTGGTTGGACTGCAGCAATGGATACA
534 K L S K N T V T D D I L C T S P G H L D
1621 AAAGTTAAGCAAGAACACAGTGACAGATGACATCCTCTGCACTTCCCCCGGGCATCTCGA
554 K K E L K A L N S E I L C P G L V N N P
1681 CAAAAGGAATTGAAAGCCCTAAATAGTGAAATTCTCTGTCCAGGTTTAGTAAATAACCC
574 S M P T Q T S Y L M V T T P A T T T N T
1741 ATCCATGCCAACACAGACTAGTTACCTTATGGTCACCACTCCTGCAACAACAACAATAC
594 A D T I L R S L T D A V P L S V L I L G
1801 GGCTGATACTATTTTACGATCTCTTACGGACGCTGTGCCACTGTCTGTTCTAATATTGGG
614 L L I M F I T I V F C A A G I V V L V L
1861 ACTTCTGATTATGTTTCATCACTATTGTTTTCTGTGCTGCAGGGATAGTGGTTCTTGTTC
634 H R R R R Y K K K Q V D E Q M R D N S P
1921 TCACCGCAGGAGAAGATACAAAAAGAAACAAGTAGATGAGCAAATGAGAGACAACAGTCC
654 V H L Q Y S M Y G H K T T H H T T E R P
1981 TGTGCATCTTCAGTACAGCATGTATGGCCATAAAACCACTCATCACACTACTGAAAGACC
674 S A S L Y E Q H M V S P M V H V Y R S P
2041 CTCTGCCTCACTCTATGAACAGCACATGGTGAGCCCCATGGTTCATGTCTATAGAAGTCC
694 S F G P K H L E E E E E R N E K E G S D
2101 ATCCTTTGGTCCAAAGCATCTGGAAGAGGAAGAAGAGAGGAATGAGAAAGAAGGAAGTGA
714 A K H L Q R S L L E Q E N H S P L T G S
2161 TGCAAAACATCTCCAAAGAAGTCTTTTGGAACAGGAAAATCATTCACTCACAGGGTC
734 N M K Y K T T N Q S T E F L S F Q D A S
2221 AAATATGAAATACAAAACCACGAACCAATCAACAGAATTTTTATCCTTCCAAGATGCCAG
754 S L Y R N I L E K E R E L Q Q L G I T E
2281 CTCATTGTACAGAAACATTTTAGAAAAAGAAAGGGAACCTCAGCAACTGGGAATCACAGA
774 Y L R K N I A Q L Q P D M E A H Y P G A
2341 ATACCTAAGGAAAAACATTGCTCAGCTCCAGCCTGATATGGAGGCACATTATCCTGGAGC
794 H E E L K L M E T L M Y S R P R K V L V
2401 CCACGAAGAGCTGAAGTTAATGGAAACATTAATGTACTCACGTCCAAGGAAGGTATTAGT
814 E Q T K N E Y F E L K A N L H A E P D Y
2461 GGAACAGACAAAAATGAGTATTTTGAACCTAAAGCTAATTTACATGCTGAACCTGACTA
834 L E V L E Q Q T * (SEQ ID NO:657)
2521 TTTAGAAGTCCTGGAGCAGCAACATAGatggaga (SEQ ID NO:656)

Figure 3. 158P1D7 amino acid sequence.

```
1 MKLWIHLFYS SLLACISLHS QTPVLSSRGS CDSLNCNEEK DGTMLINCEA KGIKMVSEIS
61 VPPSRPFQLS LLNNGLTMLH TNDFSGLTNA ISIH LGFN NI ADIEIGAFNG LGLLKQLHIN
121 HNSLEILKED TFHGLENLEF LQADNNFITV IEP S AFSKLN RLKVLILNDN AIESLPPNIF
181 RFVPLTHLDL RGNQLQTL PY VGFLEHIGRI LDLQLEDNKW ACNCDLLQLK TWLENMPPQS
241 IIGDVVCNSP PFFKGSILSR LKKESICPTP PVYEEHEDPS GSLHLAATSS INDSRMSTKT
301 TSILKLPTKA PGLIPYITKP STQLPGPYCP IPCNCKVLSP SGLLIHCQER NIESLSDLRP
361 PPQNPRKLIL AGNIIHSLMK SDLVEYFTLE MLHLGNNRIE VLEEGSFMNL TR LQKLYLNG
421 NHLTKLSKGM FLGLHNLEYL YLEYNAIKEI L PGTFNPMPK LKVLYLNNNL LQVLPPHIFS
481 GVPLTKVNLK TNQFTHLPVS NILDDDLLT QIDLEDNPWD CSCDLVGLQQ WIQKLSKNTV
541 TDDILCTSPG HLDKKELKAL NSEILCPGLV NNPSMPTQTS YLMVTTTATT TNTADTILRS
601 LTDAVPLSVL ILGLLIMFIT IVFCAAGIVV LVLHRRRRYK KKQVDEQMRD NSPVHLQYSM
661 YGHKTTHHTT ERPSASLYEQ H MVSPMVHVY RSPSFGPKHL EEEEEERNEKE GSDAKHLQRS
721 LLEQENHSPL TGSNMKYKTT NQSTEFLSFQ DASSLYRNIL EKERELQQLG ITEYLRKNIA
781 QLQPDMEAHY PGAHEELKLM ETLMYSRPRK VLVEQTKNEY FELKANLHAE PDYLEVLEQQ
841 T* (SEQ ID NO:657)
```

158P1D7

Figure 4. 158PID7 amino acid BLAST homology to hypothetical protein RLJ42114.

Identities = 798/798 (100%)

Query: 44 MLINCEAKGIKVMSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
 MLINCEAKGIKVMSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
 Sbjct: 1 MLINCEAKGIKVMSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

Query: 104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
 Sbjct: 61 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

Query: 164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN 223
 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN
 Sbjct: 121 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPHYVGFLEHIGRILDQLLEDNKWACN 180

Query: 224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
 Sbjct: 181 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

Query: 284 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
 Sbjct: 241 HLAATSSINDSRMSTKTTSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

Query: 344 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRRIEVLE 403
 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRRIEVLE
 Sbjct: 301 LIHCQERNIESLSDLRPPPQNPRKLILAGNIHSLMKSDLVEYFTLEMLHLGNRRIEVLE 360

Query: 404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 463
 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV
 Sbjct: 361 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLEYLYLEYNAIKEILPGTFNPMPLKV 420

Query: 464 LYLNNNLLQVLPPIHFSGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC 523
 LYLNNNLLQVLPPIHFSGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC
 Sbjct: 421 LYLNNNLLQVLPPIHFSGVPLTKVNLKTNQFTHLPVSNILDDDLLTQIDLEDNPWDCSC 480

Query: 524 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKEKALNSEILCPGLVNNPSMPTQTSYLM 583
 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKEKALNSEILCPGLVNNPSMPTQTSYLM
 Sbjct: 481 DLVGLQQWIQKLSKNTVTDDILCTSPGHLDKKEKALNSEILCPGLVNNPSMPTQTSYLM 540

Query: 584 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 643
 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ
 Sbjct: 541 VTTPATTTNTADTILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVHRRRRYKKKQ 600

Query: 644 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 703
 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE
 Sbjct: 601 VDEQMRDNSPVHLQYSMYGHKTTHHTTERPSASLYEQHMVSPMVHVYRSPSFGPKHLEEE 660

Query: 704 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 763
 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE
 Sbjct: 661 EERNEKEGSDAKHLQRSLLQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYRNILEKE 720

Query: 764 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 823
 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL
 Sbjct: 721 RELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTKNEYFEL 780

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Figure 5a: Alignment of 158P1D7 with human FLJ22774, CLONE KAIA1575. [Homo sapiens]

Identities = 405/415 (97%), Positives = 405/415 (97%)

```

158P1D7: 44 MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 103
              MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI
Sbjct: 1      MLINCEAKGIKMVSEISVPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI 60

158P1D7:104 EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 163
              EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK
Sbjct: 61     EIGAFNGLGLLKQLHINHNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLK 120

158P1D7:164 VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLEDNKWACN 223
              VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLEDNKWACN
Sbjct: 121    VLILNDNAIESLPPNIFRFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLEDNKWACN 180

158P1D7:224 CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 283
              CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL
Sbjct: 181    CDLLQLKTWLENMPPQSIIGDVVCNSPPFFKGSILSRKKESICPTPPVYEEHEDPSGSL 240

158P1D7:284 HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 343
              HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL
Sbjct: 241    HLAATSSINDSRMSTKTTSSILKLPTKAPGLIPYITKPSTQLPGPYCPIPCNCKVLSPSGL 300

158P1D7:344 LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 403
              LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE
Sbjct: 301    LIHCQERNIESLSDLRPPQNPRLILAGNIIHSLMKSDLVEYFTLEMLHLGNNRIEVLE 360

158P1D7:404 EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNPM 458
              EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLH                      AIKEILPGTFNPM
Sbjct: 361    EGSFMNLTRLQKLYLNGNHLTKLSKGMFLGLHNLLEYLYLEYNAIKEILPGTFNPM 415 (SEQ ID
NO:659)

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Figure 5b: Alignment of 158P1D7 protein with a human protein similar to IGFALS

Identities = 316/864 (36%), Positives = 459/864 (52%)

```

158P1D7:1  MKLWIHLFYSSLLACISLHSQTPVLSSRGSCDSLNCCEKDGTMLINCEAKGIKMVSEIS 60
              M LW+ L S+L++ + S V ++C+C + + +NCE + +++
Sbjct: 17   MFLWLFLILSALISSTNADSDISV-----EICNVCSCSVSENVLYVNCVKSVYRPNQLK 71

158P1D7:61 VPPSRPFQSLNNGLTMLHTNDFSGLTNAISIHGFGNNIADI EIGAFNGLGLLKQLHIN 120
              P S + L+ NN L +L+ N F ++A+S+HLG N + +IE GAF GL LKQLH+N
Sbjct: 72   PPWSNFYHLNFQNNFLNILYPNTFLNFSHA VSLHLGNNKLQNI EGGAFLGLSALKQLHLN 131

158P1D7:121 HNSLEILKEDTFHGLENLEFLQADNNFITVIEPSAFSKLNRLKVLILNDNAIESLPPNIF 180
              +N L+IL+ DTF G+ENLE+LQAD N I IE AF+KL++LKV LILNDN I LP NIF
Sbjct: 132  NNELKILRADTFGLGIENLEYLQADYNLIK YIERGAFNKLHKLKVLILNDNLISFLPDNIF 191

158P1D7:181 RFVPLTHLDLRGNQLQTLPLYVGFLHIGRILDQLEDNKWACNCDLLQLKTWLENMPPQS 240
              RF LTHLD+RGN++Q LPY+G LEHIGR+++LQLEDN W C+CDLL LK WLENMP
Sbjct: 192  RFASLTHLDIRGNRIQKLPYIGVLEHIGRVVELQLEDNPWNCSCDLLPLKAWLENMPYNI 251

158P1D7:241 IIGDVVCNSPPFFKGSILSRKKESICP-----TPPVYEEHEDPSGSLHLAATS 289
              IG+ +C +P G +L K+ +CP PP E+ + + H TS
Sbjct: 252  YIGEACETPSDLYGRLLKETNKQELCPMGTGSDFDVRILPPSQLENGYTTPNGHTTQTS 311

158P1D7:290 SINDSRMSTKTTSSILKLPTKAPGLI-----PYITKPSTQLPG-PYCPIPCNCVK- 337
              KTT+ P+K G++ I T++P CP PC CK
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158P1D7:338 LSPSGLLIHCQERNIESLSDLRPPPPQNPRKLILAGNIIHSLMKSDLVEYFTLEMLHLGNN 397
S GL ++CQE+NI+S+S+L P P N +KL + GN I + SD ++ L++LHLG+N
Sbjct: 368 PSDLGLSVNCQEKNIQSMSELIPKPLNAKHLHVNGNSIKDQVDVSDFTDFEGLDLLHLGNS 427

158P1D7:398 RIEVLEEGSFNNLTRLQKLYLNGNHLTKLSKGMFLGLHXXXXXXXXXXAIKEILPGTFNP 457
+I V++ F NLT L++LYLNGN + +L +F GLH IKEI GTF+
Sbjct: 428 QITVIKGDVFNLTNLRRLYLNGNQIERLYPEIFSGLHNLQYLYLEYNLIKEISAGTFDS 487

158P1D7:458 MXXXXXXXXXXXXXXXXXXHIFSGVPLTKVNLKTNQFTHLPVSNIXXXXXXXXXXXXXXN 517
M +IFSG PL ++NL+ N+F +LPVS + N
Sbjct: 488 MPNLQLLYLNNLLKSLPVYIFSGAPLARLNLNRNKFMYLPVSGVLDQLQSLTQIDLEGN 547

158P1D7:518 PWDCSCDLVGLQWQIQLSKNTVTDDILCTSPGHLDKKELKALNSEILCPGLVNNPSMPT 577
PWDC+CDLV L+ W++KLS V ++ C +P ELK+L +EILCP L+N PS P
Sbjct: 548 PWDCTCDLVALKLWVEKLSGDIVVKELKCETPVQFANIELKSLKNEILCPKLLNKPSAP- 606

158P1D7:578 QTSYLMVXXXXXXXXXXXXXILRSLTDAVPLSVLILGLLIMFITIVFCAAGIVVLVLRHR 637
+ I VPLS+LIL +L++ I VF A ++V VL R +
Sbjct: 607 ---FTSPAPAITFTTLPGLPIRSPPGGPVPLSILILSVLVLILTVFVAFCLLVFVLRNRK 663

158P1D7:638 RYKKKQVDEQMRDNSPVHLQYSMYGHKTTHTTTERPSASLYEQHMVSPMVHVYRSPSFGP 697
+ K D + LQ + HK T + E + + +S + G
Sbjct: 664 KPTVKHEGLGNPDCGSMQLQLRKHDHK-----TNKKDGLSTEAFIPQTIEQMSKSHTCGL 718

158P1D7:698 KHLXXXXXXXXXXGSDAKHLQRSLEQENHSPLTGSNMKYKTTNQSTEFLSFQDASSLYR 757
K G K + R++ ++E + + T ++ E +D++ +
Sbjct: 719 KESETGFMFSDPPGQ--KVVMRNVADKEKDLLHVDTRKRLSTIDELDELFPSSRDSNVFIQ 776

158P1D7:758 NILEKERELQQLGITEYLRKNIAQLQPDMEAHYPGAHEELKLMETLMYSRPRKVLVEQTK 817
N LE ++E +G++ + E YP + K ++L+ K++VEQ K
Sbjct: 777 NFLESKKEYNSIGVSGF-----EIRYPEKQPDKKSKSLIGGNHISKIVVEQRK 824

158P1D7:818 NEYFELKANLHAEPDYLEVLEQQT 841
+EYFELKA L + PDYL+VLE+QT
Sbjct: 825 SEYFELKAKLQSSPDYLVLEEQT 848 (SEQ ID NO:660)

Title: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 158P1D7
USEFUL IN THE TREATMENT AND DETECTION OF BLADDER AND
OTHER CANCERS
First Inventor: Mary FARIS, et al.
Application No.: To be assigned
Docket No.: 51158-20050.00
Sheet 8 of 20

Figure 6. Expression of 158P1D7 by RT-PCR

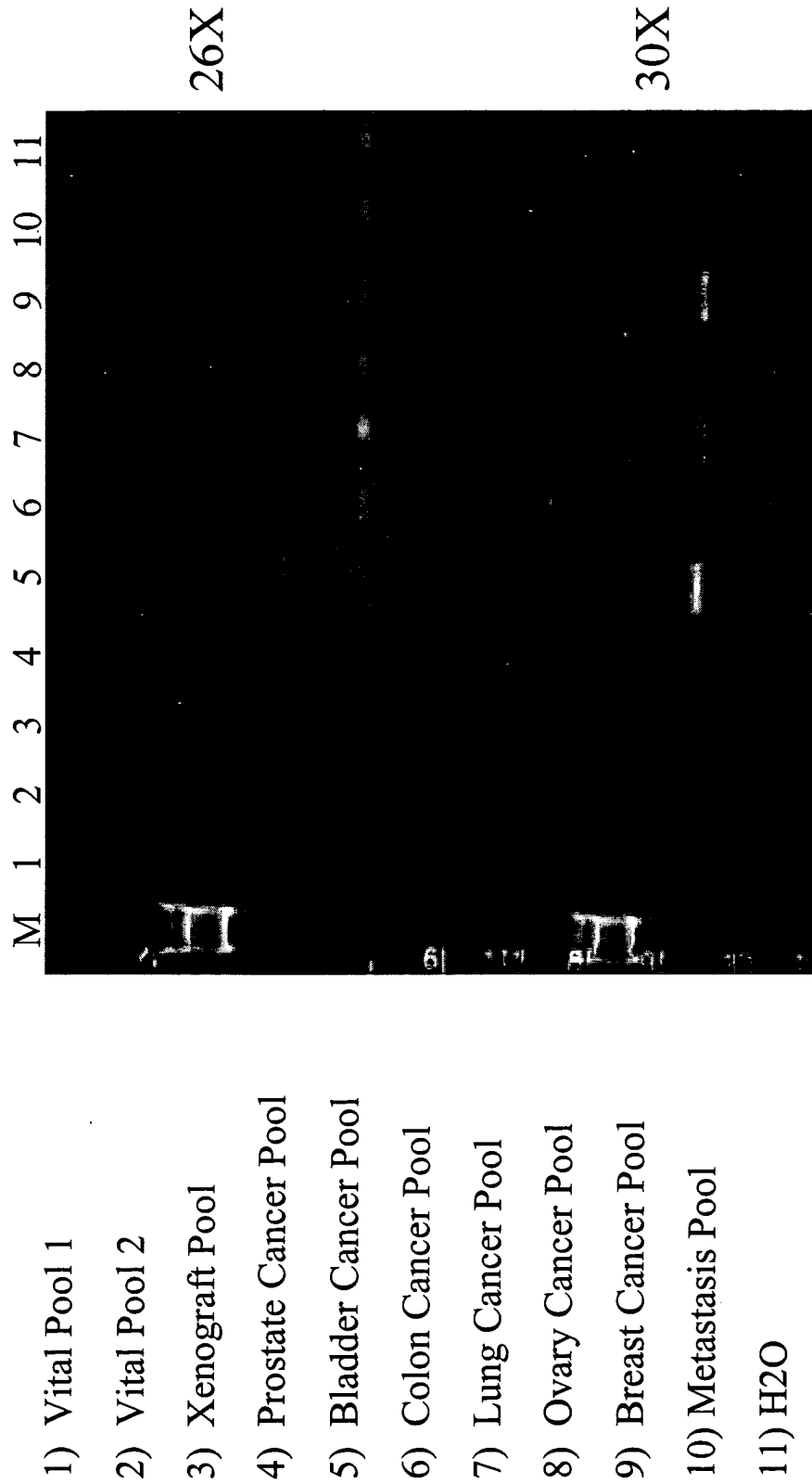


Figure 7. Expression of 158P1D7 in Normal Tissues

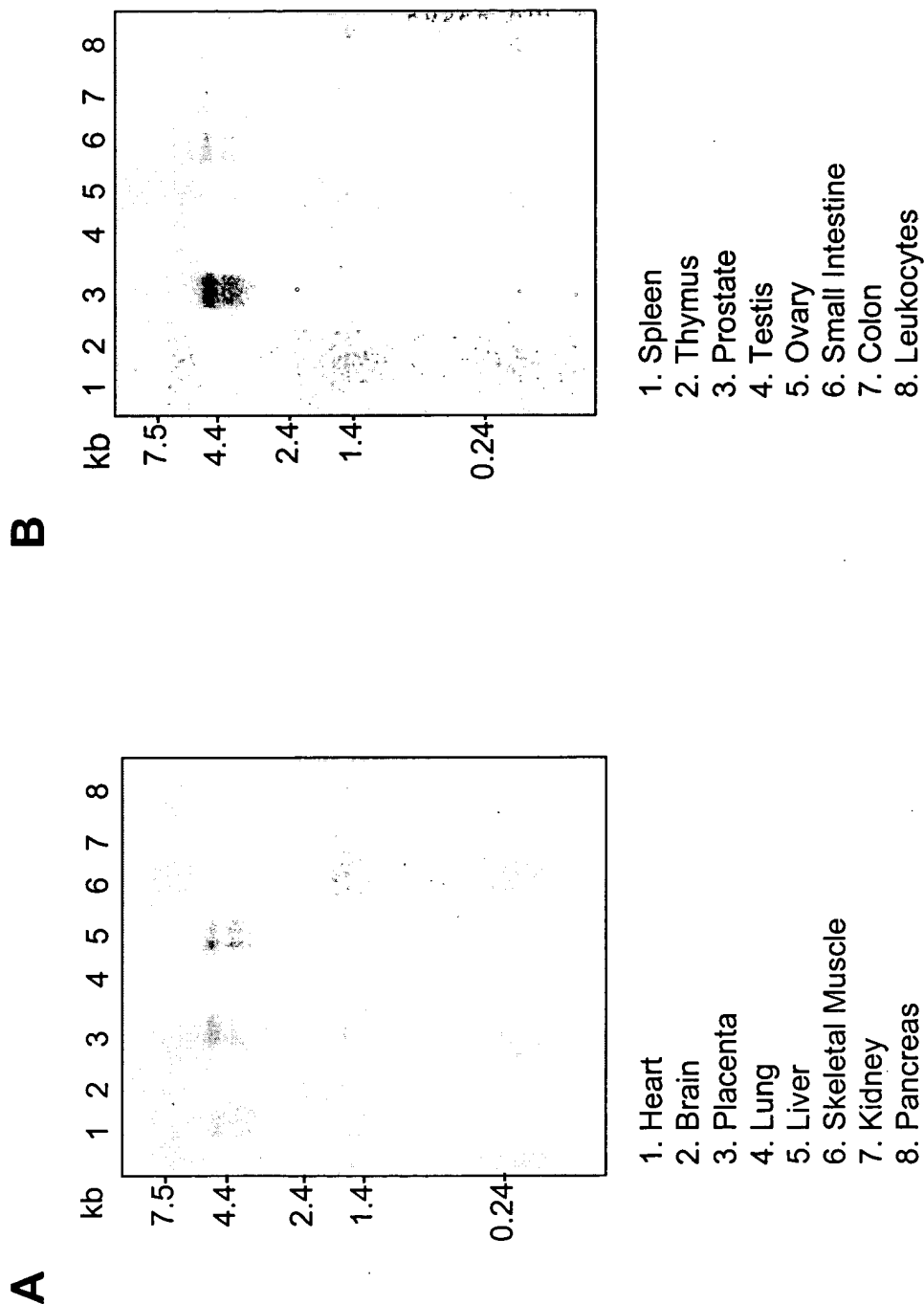
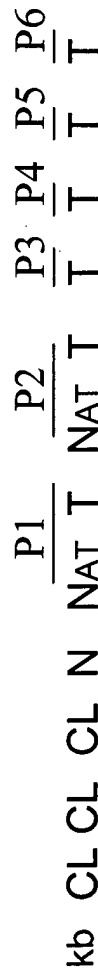


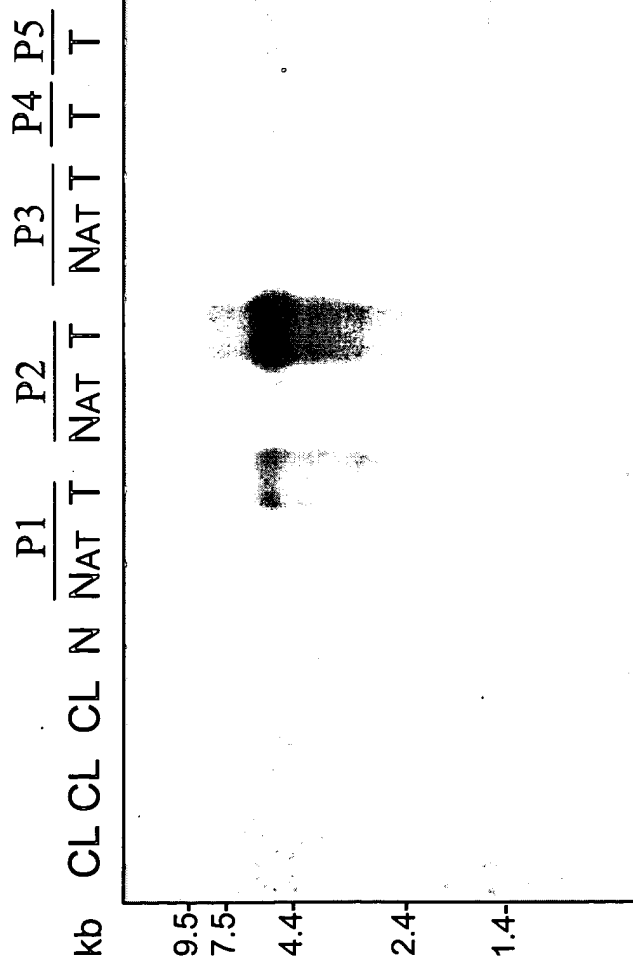
Figure 8A. Expression of 158P1D7 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 4
P2 - Squamous inv.
P3 - Transitional, grade 3
P4 - Papillary non-inv, grade 3
P5 - Papillary, grade 3/3
P6 - Transitional, grade 3/2

CL = Cell lines (listed in order): UM-UC-3, J82, ScaBER
P = Patient
N = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

Figure 8B. Expression of 158P1D7 in Bladder Cancer Patient Specimens



P1 - Transitional, grade 2
P2 - Transitional, grade 3/2
P3 - Transitional,
P4 - Polypoid Cystitis
P5 - Papillary, grade 3/3

CL = Cell lines (from left to right):
UM-UC-3, J82, SCaBER
P = Patient
N = Normal Bladder
NAT = Normal adjacent tissue
T = Tumor

Figure 9. Expression of 158P1D7 in Lung Cancer Patient Specimens

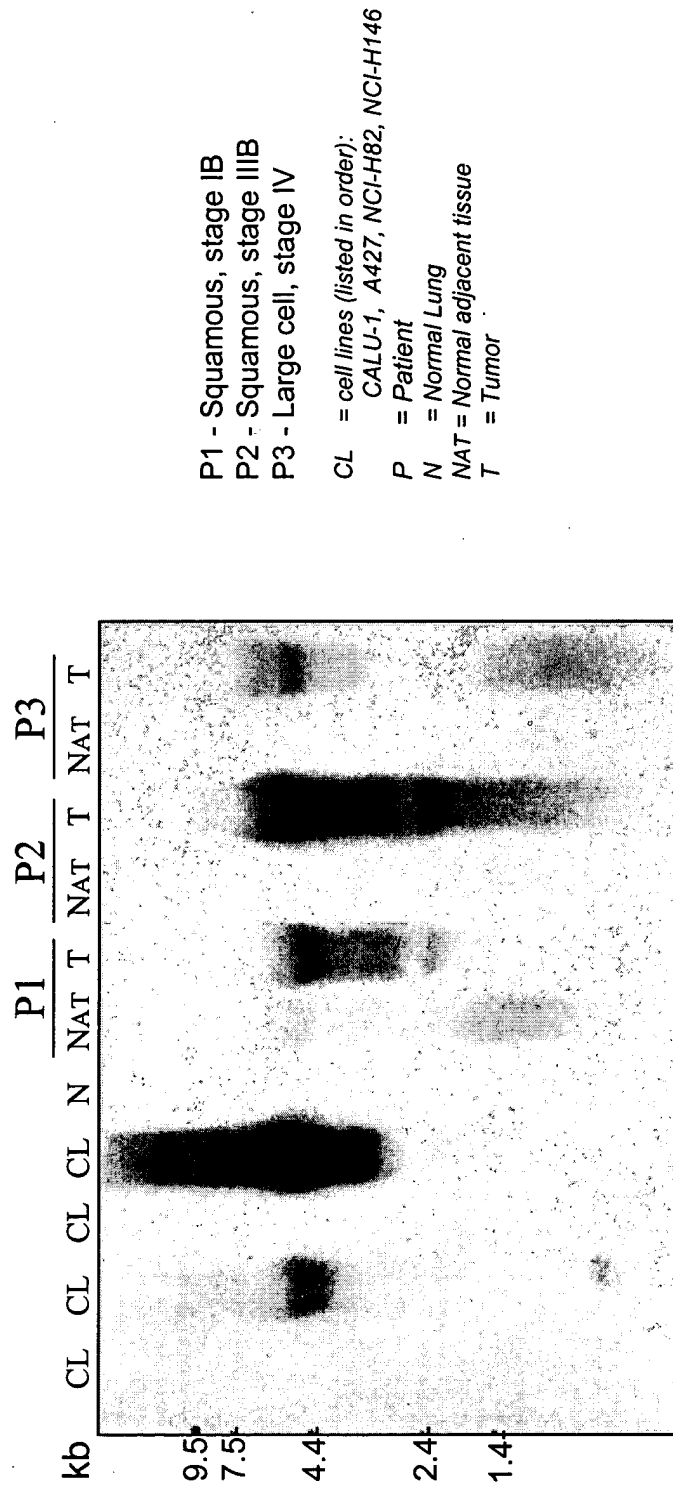


Figure 10. Expression of 158P1D7 in Breast Cancer Patient Specimens

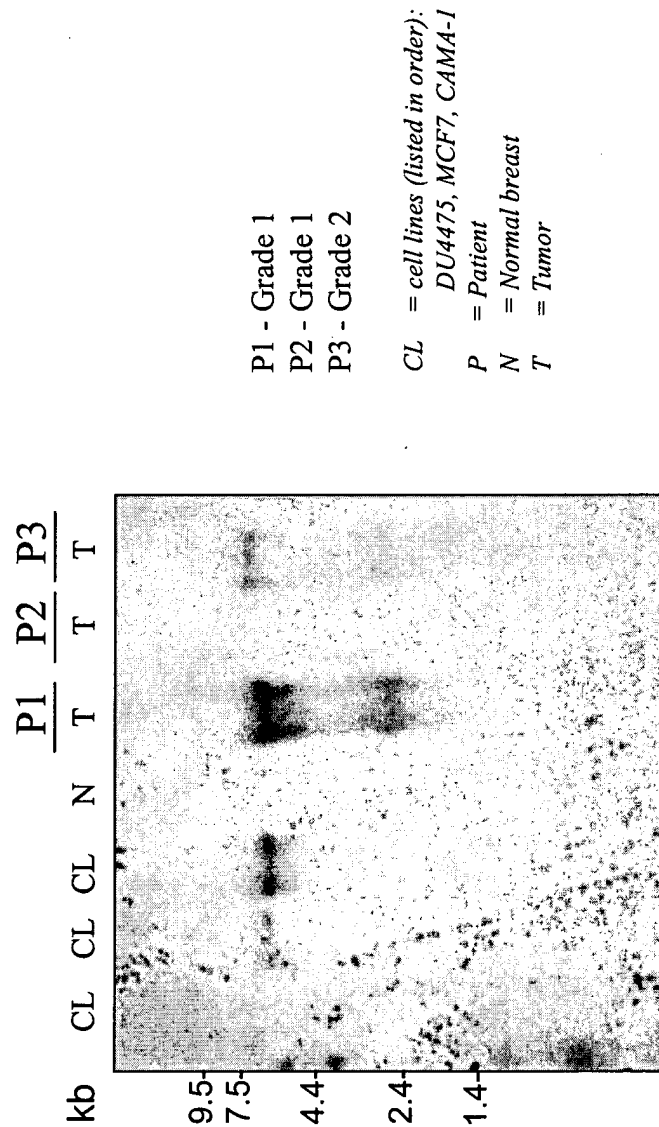


Figure 11. 158P1D7 Hydrophilicity profile
(Hopp T.P., Woods K.R., 1981. Proc. Natl. Acad. Sci. U.S.A. 78:3824-3828)

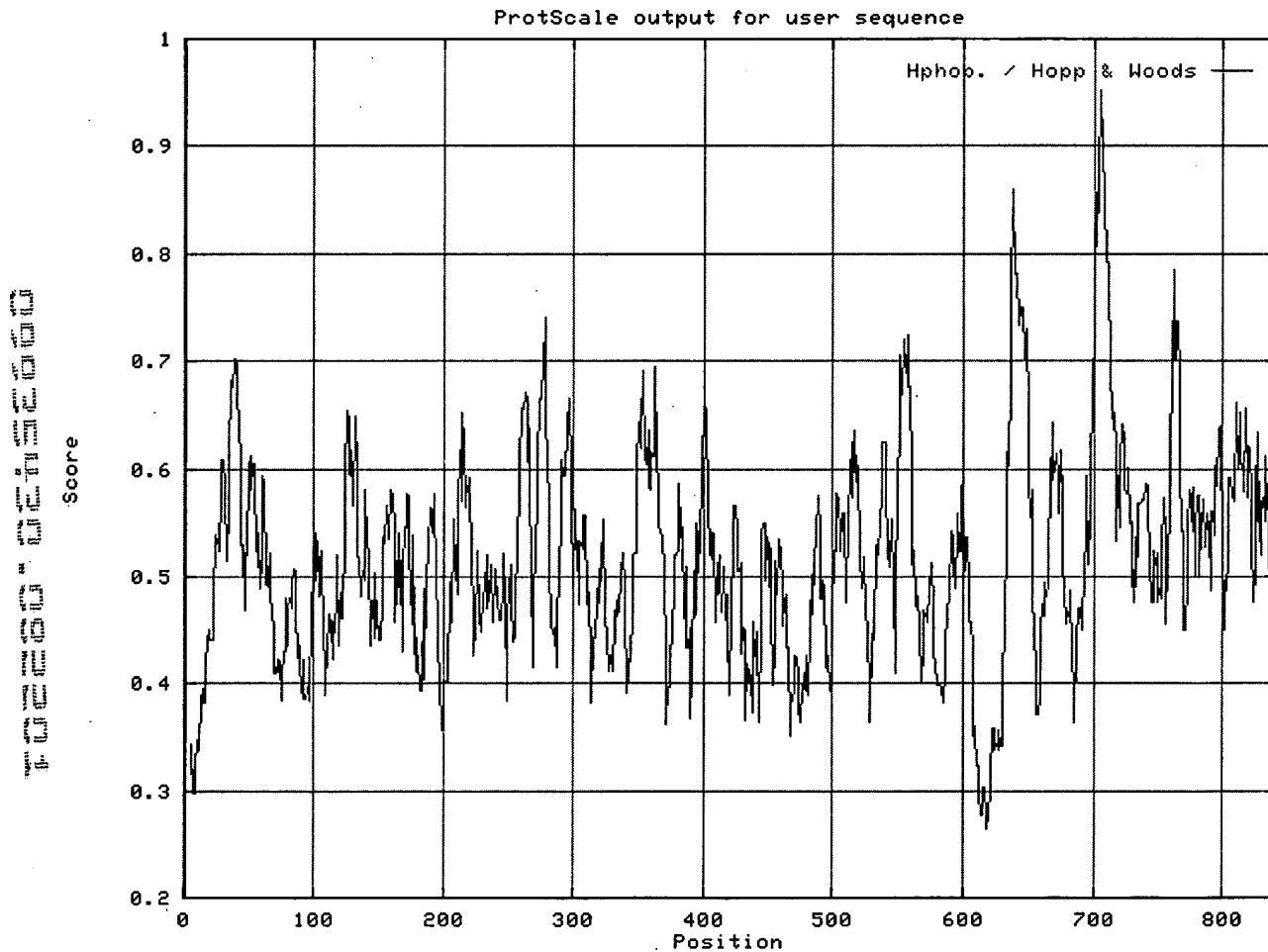


Figure 12. 158P1D7 Hydropathicity Profile
(Kyte J., Doolittle R.F., 1982. J. Mol. Biol. 157:105-132)

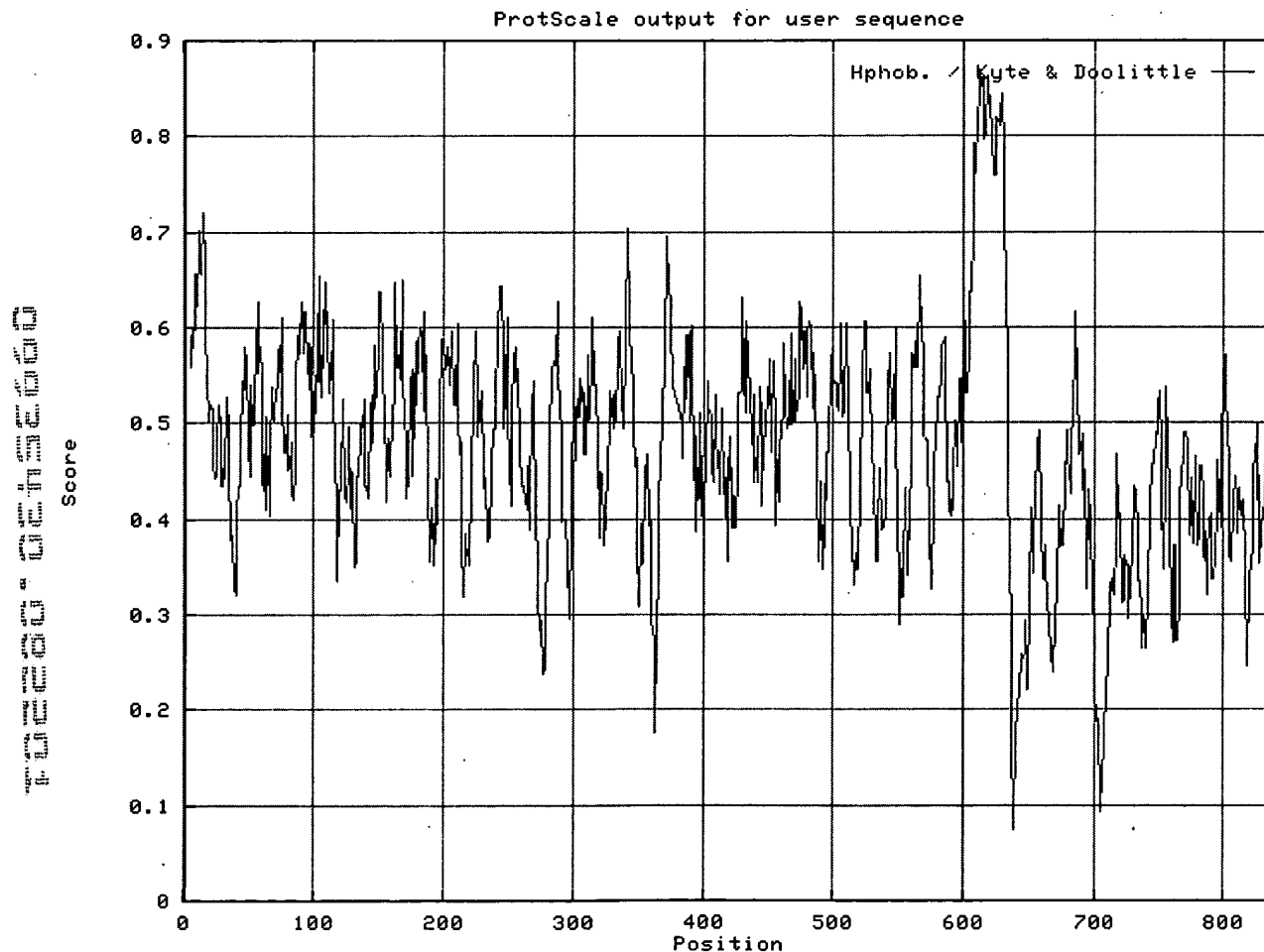


Figure 13. 158P1D7 % Accessible Residues Profile
(Janin J., 1979. Nature 277:491-492)

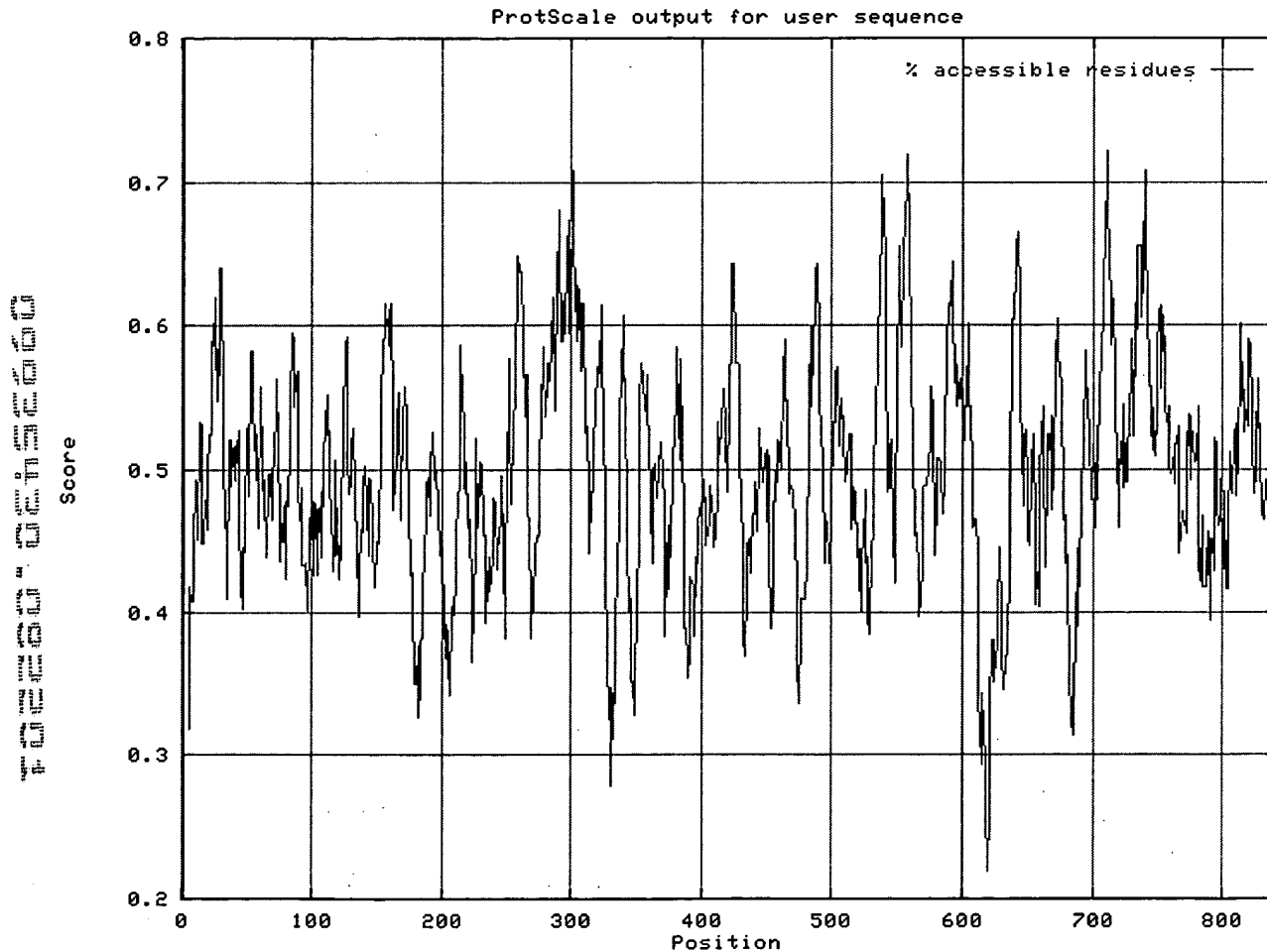


Figure 14. 158P1D7 Average Flexibility Profile

(Bhaskaran R., Ponnuswamy P.K., 1988.

Int. J. Pept. Protein Res. 32:242-255)

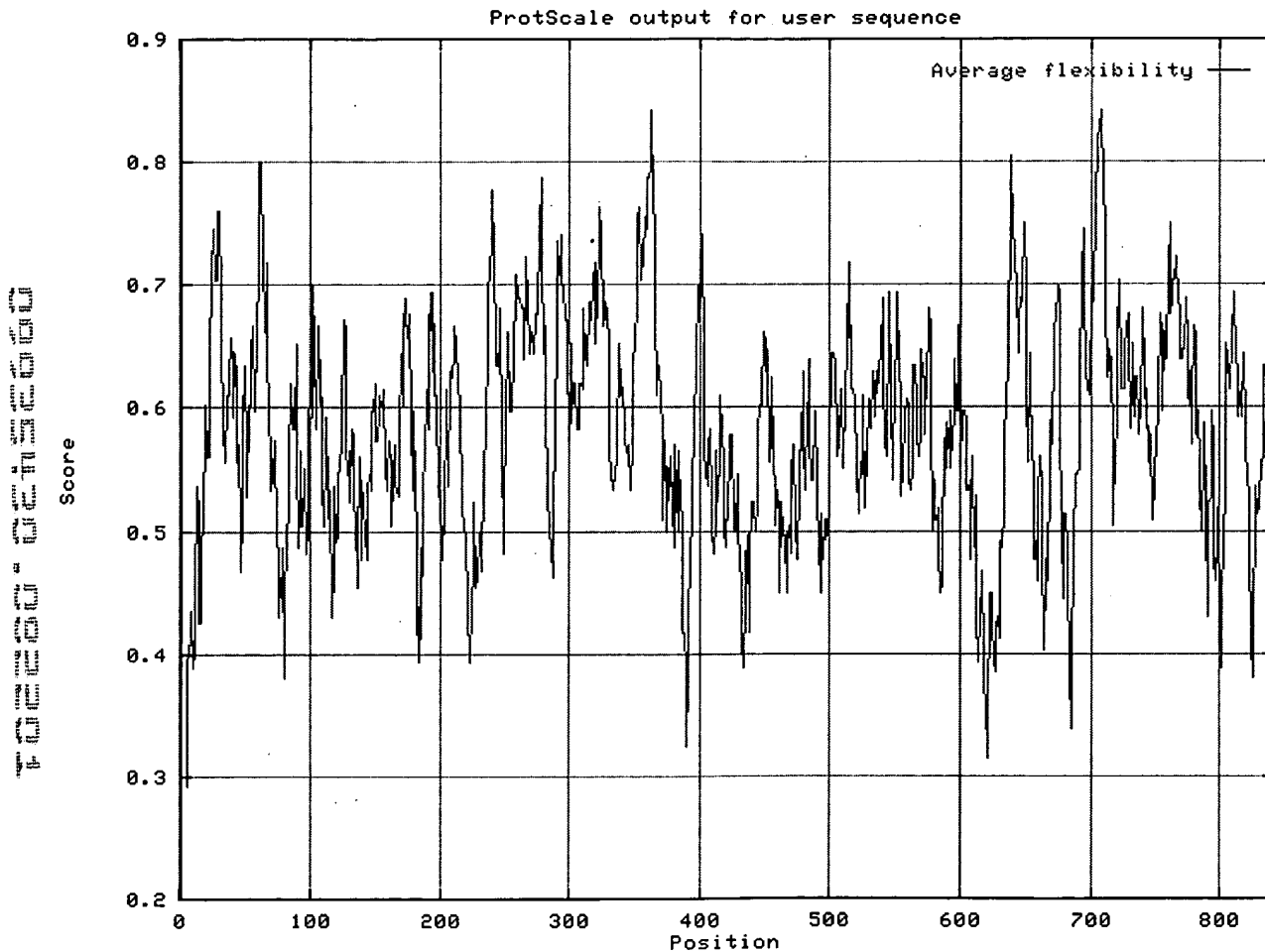
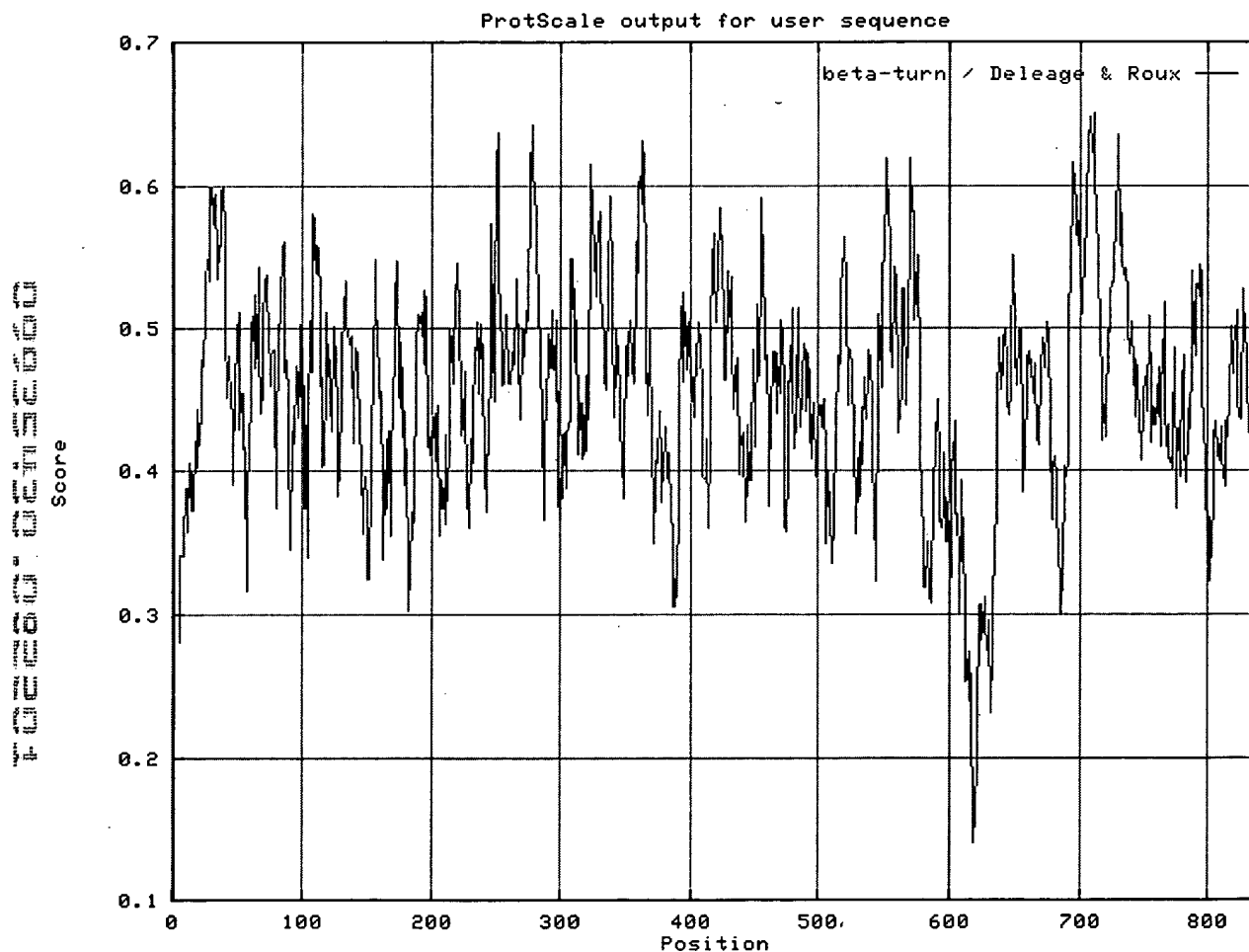
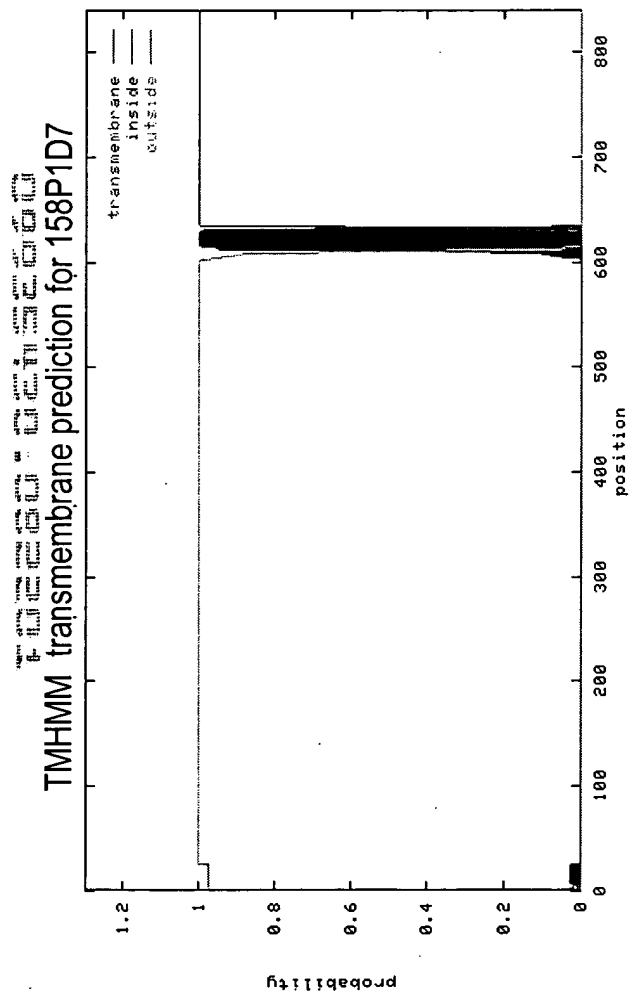


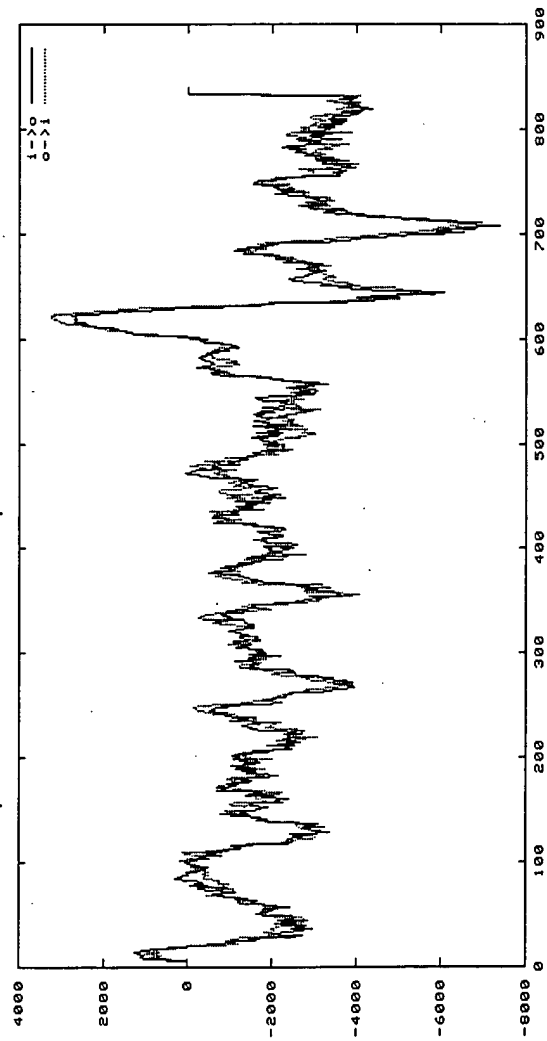
Figure 15. 158P1D7 Beta-turn Profile
(Deleage, G., Roux B. 1987. Protein Engineering 1:289-294)



16A



TMpred transmembrane prediction for 158P1D7



16B